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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/961,201

DATE: 12/07/2001  
TIME: 12:18:52

Input Set : N:\Crf3\RULE60\09961201.txt  
Output Set: N:\CRF3\12072001\I961201.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: DIXIT, VISHVA M.

6 HE, WEI-WU

7 KIKLY, KRISTINE K.

8 RUBEN, STEVEN M.

10 (ii) TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING

11 ENZYME LIKE APOPTOTIC PROTEASE-6

13 (iii) NUMBER OF SEQUENCES: 11

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Ratner &amp; Prestia

17 (B) STREET: P.O. Box 980

18 (C) CITY: Valley Forge

19 (D) STATE: PA

20 (E) COUNTRY: USA

21 (F) ZIP: 19482

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Diskette

25 (B) COMPUTER: IBM Compatible

26 (C) OPERATING SYSTEM: DOS

27 (D) SOFTWARE: FastSEQ for Windows Version 2.0

29 (vi) CURRENT APPLICATION DATA:

C--&gt; 30 (A) APPLICATION NUMBER: US/09/961,201

C--&gt; 31 (B) FILING DATE: 24-Sep-2001

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 09/300,328

37 (B) FILING DATE:

39 (A) APPLICATION NUMBER: US/08/852,936

40 (B) FILING DATE: 08-MAY-1997

42 (A) APPLICATION NUMBER: 60/018,961

43 (B) FILING DATE: 05-JUN-1996

45 (A) APPLICATION NUMBER: 60/020,344

46 (B) FILING DATE: 23-MAY-1996

48 (A) APPLICATION NUMBER: 60/017,949

49 (B) FILING DATE: 20-MAY-1996

51 (viii) ATTORNEY/AGENT INFORMATION:

52 (A) NAME: Prestia, Paul F

53 (B) REGISTRATION NUMBER: 23,031

54 (C) REFERENCE/DOCKET NUMBER: p50483-2

56 (ix) TELECOMMUNICATION INFORMATION:

57 (A) TELEPHONE: 610-407-0700

58 (B) TELEFAX: 610-407-0700

59 (C) TELEX: 846169

62 (2) INFORMATION FOR SEQ ID NO: 1:

64 (i) SEQUENCE CHARACTERISTICS:

65 (A) LENGTH: 416 amino acids

ENTERED

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66          (B) TYPE: amino acid
67          (C) STRANDEDNESS: single
68          (D) TOPOLOGY: linear
70      (ii) MOLECULE TYPE: protein
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74 Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
75   1          5          10          15
76 Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg
77          20          25          30
78 Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
79          35          40          45
80 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
81          50          55          60
82 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
83          65          70          75          80
84 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly
85          85          90          95
86 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
87          100          105          110
88 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
89          115          120          125
90 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
91          130          135          140
92 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
93          145          150          155          160
94 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
95          165          170          175
96 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
97          180          185          190
98 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
99          195          200          205
100 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
101          210          215          220
102 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
103          225          230          235          240
104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
105          245          250          255
106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
107          260          265          270
108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
109          275          280          285
110 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
111          290          295          300
112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
113          305          310          315          320
114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
115          325          330          335
116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
117          340          345          350

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118 Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
119           355                      360                      365
120 Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
121           370                      375                      380
122 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
123           385                      390                      395                      400
124 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
125           405                      410                      415

127 (2) INFORMATION FOR SEQ ID NO: 2:
129     (i) SEQUENCE CHARACTERISTICS:
130         (A) LENGTH: 1578 base pairs
131         (B) TYPE: nucleic acid
132         (C) STRANDEDNESS: single
133         (D) TOPOLOGY: linear
135     (ii) MOLECULE TYPE: cDNA
137     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
139 GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT GGTGGAAGAG      60
140 CTGCAGGTGG ACCAGCTCTG GGACGTCTCT CTGAGCCGCG AGCTGTTTCTG GCCCCATATG     120
141 ATCGAGGACA TCCAGCGGGC AGGCTCTGGA TCTCGGCGGG ATCAGGCCAG GCAGCTGATC      180
142 ATAGATCTGG AGACTCGAGG GAGTCAGGCT CTTCTTTTGT TCATCTCCTG CTTAGAGGAC     240
143 ACAGGCCAGG ACATGCTGGC TTCGTTTCTG CGAACTAACA GGCAAGCAGG AAAGTTGTCTG     300
144 AAGCCAACCC TAGAAAACCT TACCCAGTGT GTGCTCAGAC CAGAGATTCTG CAAACCAGAG     360
145 GTTCTCAGAC CGGAAACACC CAGACCAGTG GACATTGGTT CTGGAGGATT CCGTGATGTC     420
146 GGTGCTCTTG AGAGTTTGAG GGGAAATGCA GATTTGGCTT ACATCCTGAG CATGGAGCCC     480
147 TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTCTGCC GTGAGTCCGG GCTCCGCACC     540
148 CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCGGCGTC GCTTCTCCTC GCTGCATTTT     600
149 ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT GCTGGAGCTG     660
150 GCGCGGCAGG ACCACGGTGC TCTGGACTGC TGCGTGGTGG TCATTCTCTC TCACGGCTGT     720
151 CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGATG CCCTGTGTCTG     780
152 GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC     840
153 AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC     900
154 TCCAATTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC CACCCCGTTC     960
155 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT    1020
156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCAAGAGT    1080
157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC    1140
158 CTGCAGTCCC TCCTGCTTAG GGTGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAACAG    1200
159 ATGCCTGGTT GCTTTAATTT CCTCCGAAA AAACTTTCTT TAAAACATC ATAAGGCCAG    1260
160 GGCCCCCTAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG    1320
161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT    1380
162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT    1440
163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT    1500
164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA    1560
165 CCTCTGCACT ACTGACAT                                     1578

167 (2) INFORMATION FOR SEQ ID NO: 3:
169     (i) SEQUENCE CHARACTERISTICS:
170         (A) LENGTH: 639 base pairs
171         (B) TYPE: nucleic acid
172         (C) STRANDEDNESS: single
173         (D) TOPOLOGY: linear

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175      (ii) MOLECULE TYPE: cDNA
177      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
179 CTGACTGCCA AGAAAATGGT GCTGGCTTTG CTGGAGCTGG CGCGGCAGGA CCACGGTGCT      60
180 CTGGACTGCT GCGTGGTGGT CATTCTCTCT CACGGCTGTC AGGCCAGCCA CCTGCAGTTC      120
181 CCAGGGGCTG TCTACGGCAC AGATGGATGC CCTGTGTCGG TCGAAAAGAT TGTGAACATC      180
182 TTCAATGGGA CCAGCTGCCC CAGCCTGGGA GGGAAGCCCA AGCTCTTTT CATCCAGGCC      240
183 TGTGGTGGGG AGCAGAAAGA CCATGGGTTT GAGGTGGCCT CCACTTCCCC TGAAGACGAG      300
184 TCCCCTGGCA GTAACCCCGA GCCAGATGCC ACCCGTTCC AGGAAGGTTT GAGGACCTTC      360
185 GACCAGCTGG ACGCCATATC TAGTTTGGCC ACACCCAGTG ACATCTTTGT GTCCTACTCT      420
186 ACTTTCCCAG GTTTTGTTTC CTGGAGGGAC CCCAAGAGTG GTCCTGGTA CGTTGAGACC      480
187 CTGGACGACA TCTTTGAGCA GTGGGCTCAC TCTGAAGACC TGCAGTCCCT CCTGCTTAGG      540
188 GTCGCTAATG CTGTTTCGGT GAAAGGGATT TATAAACAGA TGCCTGGTTG CTTTAATTTT      600
189 CTCCGAAAAA AACTTTTCTT TTAACATC ATAAGGCAG      639
191 (2) INFORMATION FOR SEQ ID NO: 4:
193      (i) SEQUENCE CHARACTERISTICS:
194          (A) LENGTH: 203 amino acids
195          (B) TYPE: amino acid
196          (C) STRANDEDNESS: single
197          (D) TOPOLOGY: linear
199      (ii) MOLECULE TYPE: protein
201      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
203 Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu
204   1           5           10           15
205 Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His
206           20           25           30
207 Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser
208           35           40           45
209 Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu
210           50           55           60
211 Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln
212           65           70           75           80
213 Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser
214           85           90           95
215 Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu
216           100          105          110
217 Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser
218           115          120          125
219 Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg
220           130          135          140
221 Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe
222           145          150          155          160
223 Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val
224           165          170          175
225 Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys
226           180          185          190
227 Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met
228           195          200
230 (2) INFORMATION FOR SEQ ID NO: 5:
232      (i) SEQUENCE CHARACTERISTICS:

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```

233      (A) LENGTH: 34 base pairs
234      (B) TYPE: nucleic acid
235      (C) STRANDEDNESS: single
236      (D) TOPOLOGY: linear
238      (ii) MOLECULE TYPE: cDNA
240      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
242 GAACGGGGTA CCGCCATGGA CGAAGCGGAT CGGC
244 (2) INFORMATION FOR SEQ ID NO: 6:
246      (i) SEQUENCE CHARACTERISTICS:
247          (A) LENGTH: 60 base pairs
248          (B) TYPE: nucleic acid
249          (C) STRANDEDNESS: single
250          (D) TOPOLOGY: linear
252      (ii) MOLECULE TYPE: cDNA
254      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
256 TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTAA AAGAAAAGTT TTTTCCGGAG
258 (2) INFORMATION FOR SEQ ID NO: 7:
260      (i) SEQUENCE CHARACTERISTICS:
261          (A) LENGTH: 41 base pairs
262          (B) TYPE: nucleic acid
263          (C) STRANDEDNESS: single
264          (D) TOPOLOGY: linear
266      (ii) MOLECULE TYPE: cDNA
268      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
270 AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C
272 (2) INFORMATION FOR SEQ ID NO: 8:
274      (i) SEQUENCE CHARACTERISTICS:
275          (A) LENGTH: 39 base pairs
276          (B) TYPE: nucleic acid
277          (C) STRANDEDNESS: single
278          (D) TOPOLOGY: linear
280      (ii) MOLECULE TYPE: cDNA
282      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
284 GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC
286 (2) INFORMATION FOR SEQ ID NO: 9:
288      (i) SEQUENCE CHARACTERISTICS:
289          (A) LENGTH: 66 base pairs
290          (B) TYPE: nucleic acid
291          (C) STRANDEDNESS: single
292          (D) TOPOLOGY: linear
294      (ii) MOLECULE TYPE: cDNA
296      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
298 TGCTCTAGAT TACTTGTCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTTT
299 CCGGAG
301 (2) INFORMATION FOR SEQ ID NO: 10:
303      (i) SEQUENCE CHARACTERISTICS:
304          (A) LENGTH: 5 amino acids
305          (B) TYPE: amino acid
306          (C) STRANDEDNESS: single

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/961,201

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Input Set : N:\Crf3\RULE60\09961201.txt

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]